

ABSTRACT

The present invention relates to a method for determining HIV-1 subtypes, characterized by comprising 5 the steps of amplifying nucleic acid using as a target sequence a portion of a nucleotide sequence of the env gene of HIV-1, where at least one of the 5' terminal and 3' terminal nucleotide sequences is different depending on the HIV-1 subtype, and detecting the subtype depending on 10 whether or not the nucleic acid has been amplified. The present invention also relates to a kit for determining HIV-1 subtypes, comprising primer pairs in which a target sequence is a portion of a nucleotide sequence of the env gene of HIV-1, where at least one of the 5' terminal and 15 3' terminal nucleotide sequences is different depending on the subtype.

SEARCHED  
INDEXED  
SERIALIZED  
FILED